

RAW SEQUENCE LISTING

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Application Serial Number: 101531,415
Source: PCT
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PATENT APPLICATION: US/10/531,415

DATE: 02/22/2006

TIME: 08:25:12

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Output Set: N:\CRF4\02222006\J531415.raw

5 <110> APPLICANT: BERDEL, Wolfgang
 6 MULLER-TIDOW, Carsten
 7 SERVE, Hubert
 8 STEFFEN, Bjorn
 10 <120> TITLE OF INVENTION: Delocalization Molecules and Use Thereof
 12 <130> FILE REFERENCE: 20057.002
 14 <140> CURRENT APPLICATION NUMBER: US 10/531,415
C--> 15 <141> CURRENT FILING DATE: 2005-04-15
 17 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/011525
 18 <151> PRIOR FILING DATE: 2003-10-17
 20 <150> PRIOR APPLICATION NUMBER: DE 102 48 751.0
 21 <151> PRIOR FILING DATE: 2002-10-18
 23 <160> NUMBER OF SEQ ID NOS: 13
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 497
 29 <212> TYPE: PRT
 30 <213> ORGANISM: artificial sequence
 32 <220> FEATURE:
 33 <223> OTHER INFORMATION: Amino acid sequence of GFP-M&M
 35 <400> SEQUENCE: 1
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 38 1 5 10 15
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 42 20 25 30
 45 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 46 35 40 45
 49 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 50 55 60
 53 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 54 65 70 75 80
 57 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 58 85 90 95
 61 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 62 100 105 110
 65 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 66 115 120 125
 69 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 70 130 135 140
 73 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 74 145 150 155 160
 77 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
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81 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 82 180 185 190
 85 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 86 195 200 205
 89 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 90 210 215 220
 93 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Gly
 94 225 230 235 240
 97 Thr Val Ile Ala Asn Tyr Leu Pro Asn Arg Thr Asp Val Gln Cys Gln
 98 245 250 255
 101 His Arg Trp Gln Lys Val Leu Asn Pro Glu Leu Ile Lys Gly Pro Trp
 102 260 265 270
 105 Thr Lys Glu Glu Asp Gln Arg Val Ile Glu Leu Val Gln Lys Tyr Gly
 106 275 280 285
 109 Pro Lys Arg Trp Ser Val Ile Ala Lys His Leu Lys Gly Arg Ile Gly
 110 290 295 300
 113 Lys Gln Cys Arg Glu Arg Trp His Asn His Leu Asn Pro Glu Val Lys
 114 305 310 315 320
 117 Lys Thr Ser Trp Thr Glu Glu Glu Asp Arg Ile Ile Tyr Gln Ala His
 118 325 330 335
 121 Lys Arg Leu Gly Asn Arg Trp Ala Glu Ile Ala Lys Leu Leu Pro Gly
 122 340 345 350
 125 Arg Thr Asp Asn Ala Ile Lys Asn His Trp Asn Ser Thr Met Arg Arg
 126 355 360 365
 129 Lys Val Glu Gln Glu Gly Tyr Gly Ser Ala Thr Ser His Thr Met Ser
 130 370 375 380
 133 Thr Ala Glu Val Leu Leu Asn Met Glu Ser Pro Ser Asp Ile Leu Asp
 134 385 390 395 400
 137 Glu Lys Gln Ile Phe Ser Thr Ser Glu Met Leu Pro Asp Ser Asp Pro
 138 405 410 415
 139 Ala Pro Ala Val Thr Leu Pro Asn Tyr Leu Phe Pro Ala Ser Glu Pro
 140 420 425 430
 143 Asp Ala Leu Asn Arg Ala Gly Asp Thr Ser Asp Gln Glu Gly His Ser
 144 435 440 445
 147 Leu Glu Glu Lys Ala Ser Arg Glu Glu Ser Ala Lys Lys Thr Gly Lys
 148 450 455 460
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 152 465 470 475 480
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 166 <213> ORGANISM: artificial sequence
 168 <220> FEATURE:
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 171 <400> SEQUENCE: 2
 173 atggtgagca agggcgagga gctgttcacc ggggtggc ccatcctggt cgagctggac 60

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179 ctcgtgacca ccctgaccta cggcggtcag tgcttcagcc gctaccccgaa ccacatgaag	240
181 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg caccatcttc	300
183 ttcaaggacg acggcaacta caagacccgc gccgaggtga agttcgaggg cgacaccctg	360
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189 ggcatcaagg tgaacttcaa gatccgcccc aacatcgagg acggcagcgt gcagctcgcc	540
191 gaccactacc agcagaacac ccccatcgcc gacggccccc tgctgctgcc cgacaaccac	600
193 tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcga tcacatggtc	660
195 ctgctggagt tcgtgaccgc cgccgggatc actctcgca tggacgagct gtacaagggt	720
197 accgtcattt ccaatttatct gcccaaccgg acagatgtgc agtgccaaca ccgtggcag	780
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203 gggagaattt gaaagcagtgc tcgggagagg tggcacaacc atttgaatcc agaagtttaag	960
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213 gagaaggcaga tcttcagtttac ctccgaaatg cttccagact cggaccctgc accagctgtc	1260
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217 actagtgacc aggagggca ttctctggag gagaaggcct ccagagagga aagtgc当地 aag	1380
219 aagactggga aatcaaagaa gagaatccgg aagaccaagg gcaaccgaag tacctcacct	1440
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 269 <223> OTHER INFORMATION: Oligonucleotide primer myb-BamHI rev
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 282 <223> OTHER INFORMATION: Oligonucleotide primer p14ARFFor
 284 <400> SEQUENCE: 7
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 335 <220> FEATURE:
 336 <223> OTHER INFORMATION: cDNA EGFP
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350	gtgcagtgtct	tcagccgcta	ccccgaccac	atgaagcagc	acgacttctt	caagtccgccc	360
352	atgcccgaag	gctacgtcca	ggagcgcacc	atcttcttca	aggacgacgg	caactacaag	420
354	accgcgcggc	aggtgaagtt	cgagggcgcac	accctggta	accgcacatcg	gctgaaggggc	480
356	atcgacttca	aggaggacgg	caacatcctg	gggcacaaga	tggagtacaa	ctacaacagc	540
358	cacaacgtct	atatcatggc	cgacaaggcag	aagaacggca	tcaagggtgaa	cttcaagatc	600
360	cggccacaaca	tcgaggacgg	cagcgtgcag	ctcgccgacc	actaccagca	gaacacccccc	660
362	atcggcgacg	gccccgtgct	gctgcccgcac	aaccactacc	tgagcaccca	gtccgccttg	720
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372	atggtttacaa	ataaaagcaat	agcatcaca	atttcacaaa	taaaggcattt	ttttcaactgc	1020
374	attcttagttt	tggtttgtcc	aaactcatca	atgtatctt	aggcgtaaat	tgttaagcggtt	1080
376	aatatttttgt	taaaatttcgc	gttaaatttt	tgttaaattca	gctcattttt	taaccaatag	1140
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